

Search Results for 10/826,170

(FILE 'HOME' ENTERED AT 16:47:44 ON 28 AUG 2006)

FILE 'REGISTRY' ENTERED AT 16:48:05 ON 28 AUG 2006

E "HDAC2"/CN 25
L1 2 S E4 OR E5
E "HISTONE DEACETYLASE 2"/CN 25
L2 2 S E4 OR E5
E "HISTONE DEACETYLASE II"/CN 25

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
16:49:41 ON 28 AUG 2006

L3 850 S L1 OR L2 OR HDAC-2 OR HDAC2
L4 5 S L3 AND CRYSTAL
L5 2 DUP REM L4 (3 DUPLICATES REMOVED)

FILE 'REGISTRY' ENTERED AT 16:51:45 ON 28 AUG 2006

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
16:52:01 ON 28 AUG 2006

L6 521 S (HISTONE (W) DEACETYLASE-2) OR (HISTONE (W) DEACETYLASE (W) 2
L7 4 S L6 AND CRYSTAL
L8 4 DUP REM L7 (0 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 16:59:31 ON 28 AUG 2006

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#13 Search #12 AND crystal	16:41:44	1
#12 Search "histone deacetylase 2" OR "histone deacetylase II"	16:40:39	114
#10 Search #2 and model	16:39:59	8
#9 Search #2 and (diffract OR diffraction)	16:38:50	0
#2 Search "histone deacetylase-2"[Substance Name]	16:38:31	96
#4 Search #2 AND structure	14:49:37	25
#3 Search #2 AND crystal	14:49:11	1

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- ☐ 4. **Regulatory role of regulatory factor for box (RFX5) complex and class II transactivator (CIITA) in the repression of the collagen alpha2(I) gene**
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- ☐ 5. **Role of DNA methyltransferase 3b in neuronal cell differentiation**
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- ☐ 6. **Analysis of human histone deacetylase 6 and its associated protein Ub190**
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- ☐ 7. **Breast cancer metastasis suppressor 1 is a component of the SIN3 histone deacetylase complex**
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- ☐ 8. **Glucose regulation of insulin gene expression**
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- ☐ 9. **Identification and characterization of a novel E2F family member, E2F7**
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10. **Post-transcriptional regulation and autoregulation of the N-myc gene in neuroblastoma**

- ☐ by Kim, Kwang-Hee (Marianne), Ph.D., Mount Sinai School of Medicine of New York University, 2004, 3115445
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- ☐ 11. **Proteins involved in transcriptional regulation on the Msx2 promoter**
 by Kang, Duk Won, M.S., University of Southern California, 2003, 95 pages; AAT 1420365
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- ☐ 12. **Protein inhibitor of activated STAT γ (PIAS γ) in androgen receptor signaling and prostate cancer**
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- ☐ 13. **Regulation of BCL6 transcriptional repressor function by p300-mediated acetylation**
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- ☐ 14. **Regulation of transcriptional repression by the mammalian Sin3 corepressor complex**
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- ☐ 16. **An analysis of mSin3A and mSin3A/Pf1/TLE transcriptional corepressor complexes**
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- ☐ 17. **Mechanisms of inactivation of von Hippel-Lindau protein in von Hippel-Lindau disease-associated tumors**
 by Sikora, Sergey I., Ph.D., University of California, Los Angeles, 2002, 134 pages; AAT 3066459
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- ☐ 18. **Molecular analysis of histone deacetylase 2**
 by Tsai, Shih-Chang, Ph.D., University of South Florida, 2002, 124 pages; AAT 3071330
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- ☐ 19. **A key strategy in Epstein-Barr virus immortalization of B lymphocytes and Notch signaling: Switching transcriptional repression to activation**
 by Zhou, Sifang, Ph.D., The Johns Hopkins University, 2001, 261 pages; AAT 3006387
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- ☐ 20. **Epigenetic control of gene expression in human cancer**
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- ☐ 21. **I. Molecular association between ATR and two components of the nucleosome remodeling and deacetylation complex, HDAC2 and CHD4. II. Construction of a synthetic library of macrolides**
 by Schmidt, Darby Rye, Ph.D., Harvard University, 2001, 152 pages; AAT 3028444
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- ☐ 22. **Characterization of the human HDAC1, HDAC2, HDAC3, and chicken erythrocyte histone deacetylase**
 by Moniwa, Mariko, M.Sc., The University of Manitoba (Canada), 2000, 116 pages; AAT MQ53197

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- ☐ 23. **Characterization of histone acetylation in butyrate-resistant HeLa cells**
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- ☐ 24. **Regulation of mammalian histone deacetylases by phosphorylation**
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Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYYDGI.....PEDAVHEDSGDEDGEDPDKR 405

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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 Listing first 45 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
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 3: geneseqp2000s:*
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 5: geneseqp2002s:*
 6: geneseqp2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2202	100.0	498	8	ADS18115	Ads18115 1-488 of
2	2202	100.0	498	9	AEA49480	Aea49480 Human his
3	2202	100.0	498	9	AEB56251	Aeb56251 Histone d
4	2198	99.8	488	5	ABB57202	Abb57202 Mouse isc
5	2184	99.2	556	6	ABO07206	Abo07206 Human p53
6	2171	98.6	488	4	AAB49955	Aab49955 Human his
7	2171	98.6	488	6	ABR47485	Abr47485 Breast ca
8	2171	98.6	488	7	ADD45711	Add45711 Human Pro
9	2171	98.6	488	7	ADE59815	Ade59815 Human Pro
10	2171	98.6	488	8	ADJ27055	Adj27055 Human his
11	2171	98.6	488	8	ADN49101	Adn49101 Human his
12	2171	98.6	488	8	ADQ20164	Adq20164 Human sof

13	2171	98.6	488	8	ADS88214	Ads88214	Human pro
14	2171	98.6	488	9	ADY70328	Ady70328	Human bet
15	2171	98.6	488	9	ADZ09732	Adz09732	Human bre
16	2171	98.6	488	10	AEF54870	Aef54870	Human his
17	2105.5	95.6	489	7	ADC21689	Adc21689	Human his
18	2105.5	95.6	489	9	ADW12269	Adw12269	Human his
19	2047.5	93.0	482	2	AAW29324	Aaw29324	A novel h
20	2047.5	93.0	482	4	AAB49954	Aab49954	Human his
21	2047.5	93.0	482	4	AAB67164	Aab67164	Human his
22	2047.5	93.0	482	6	ABO07205	Abo07205	Human p53
23	2047.5	93.0	482	8	ADJ78497	Adj78497	HDAC1 pro
24	2047.5	93.0	482	8	ADN03712	Adn03712	Antipsori
25	2047.5	93.0	482	8	ABM80055	Abm80055	Tumour-as
26	2047.5	93.0	482	8	ADS88225	Ads88225	Human pro
27	2047.5	93.0	482	9	ADX08110	Adx08110	Cyclin-de
28	2047.5	93.0	482	10	AEF54869	Aef54869	Human his
29	2047.5	93.0	488	3	AAB56985	Aab56985	Human pro
30	2047.5	93.0	513	8	ADS18113	Ads18113	1-482 of
31	2047.5	93.0	513	9	AEA49478	Aea49478	Human his
32	2047.5	93.0	513	9	AEB56249	Aeb56249	Histone d
33	2047.5	93.0	556	6	ABG72562	Abg72562	TAT dMT-H
34	2047.5	93.0	557	6	ABG72558	Abg72558	HDAC1-Tat
35	2044.5	92.8	480	8	ADO57385	Ado57385	Kidney de
36	2033.5	92.3	482	2	AAR88919	Aar88919	RPDL, a h
37	2033.5	92.3	482	5	AAE25140	Aae25140	Human his
38	2033.5	92.3	482	7	ADJ68416	Adj68416	Human hea
39	2033.5	92.3	482	7	ADN31057	Adn31057	Human his
40	2033.5	92.3	482	8	ADQ62713	Adq62713	Human his
41	2033.5	92.3	482	9	AEB95726	Aeb95726	Human His
42	2031	92.2	481	5	AAU99656	Aau99656	Human His
43	2031	92.2	481	7	ADC21687	Adc21687	Human his
44	2031	92.2	481	9	ADW12267	Adw12267	Human his
45	2022.5	91.8	482	8	ADQ62717	Adq62717	Human HDA

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Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYYDGI.....PEDAVHEDSGDEDGEDPDKR 405

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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 Listing first 45 summaries

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 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

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SUMMARIES

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		Match	Length			
1	2202	100.0	556	2	US-09-949-016-7424	Sequence 7424, Ap
2	2171	98.6	488	2	US-09-538-092-1367	Sequence 1367, Ap
3	2144	97.4	488	2	US-10-239-333B-6	Sequence 6, Appli
4	2047.5	93.0	482	2	US-09-538-092-1308	Sequence 1308, Ap
5	2047.5	93.0	482	2	US-08-624-735E-5	Sequence 5, Appli
6	2033.5	92.3	482	1	US-08-528-255A-1	Sequence 1, Appli
7	2033.5	92.3	482	1	US-08-717-365-1	Sequence 1, Appli
8	2027	92.1	481	2	US-10-239-333B-5	Sequence 5, Appli
9	2025	92.0	480	2	US-08-624-735E-10	Sequence 10, Appl
10	1985	90.1	465	2	US-09-949-016-10909	Sequence 10909, A
11	1532	69.6	439	2	US-09-282-305-6	Sequence 6, Appli
12	1532	69.6	439	2	US-09-883-720-6	Sequence 6, Appli
13	1515	68.8	517	2	US-09-282-305-8	Sequence 8, Appli
14	1515	68.8	517	2	US-09-883-720-8	Sequence 8, Appli
15	1509	68.5	493	2	US-09-720-529A-2	Sequence 2, Appli

16	1495.5	67.9	501	2	US-09-645-337A-2	Sequence 2, Appli
17	1494.5	67.9	501	2	US-09-720-529A-8	Sequence 8, Appli
18	1489.5	67.6	473	2	US-09-720-529A-4	Sequence 4, Appli
19	1483	67.3	448	2	US-09-248-796A-19163	Sequence 19163, A
20	1481	67.3	513	2	US-09-645-337A-12	Sequence 12, Appl
21	1481	67.3	513	2	US-09-720-529A-7	Sequence 7, Appli
22	1468	66.7	433	2	US-08-624-735E-9	Sequence 9, Appli
23	1468	66.7	433	2	US-09-645-337A-13	Sequence 13, Appl
24	1461.5	66.4	471	2	US-09-645-337A-4	Sequence 4, Appli
25	1416.5	64.3	428	2	US-09-538-092-828	Sequence 828, App
26	1416.5	64.3	431	2	US-09-949-016-10173	Sequence 10173, A
27	1404.5	63.8	458	2	US-09-282-305-2	Sequence 2, Appli
28	1404.5	63.8	458	2	US-09-883-720-2	Sequence 2, Appli
29	1400.5	63.6	428	2	US-10-239-333B-7	Sequence 7, Appli
30	1385	62.9	432	2	US-09-282-305-10	Sequence 10, Appl
31	1385	62.9	432	2	US-09-883-720-10	Sequence 10, Appl
32	1385	62.9	507	2	US-09-248-796A-19164	Sequence 19164, A
33	1134	51.5	454	2	US-09-248-796A-19305	Sequence 19305, A
34	1017	46.2	351	2	US-09-282-305-4	Sequence 4, Appli
35	1017	46.2	351	2	US-09-883-720-4	Sequence 4, Appli
36	829	37.6	377	2	US-10-239-333B-2	Sequence 2, Appli
37	819.5	37.2	378	2	US-10-239-333B-4	Sequence 4, Appli
38	496	22.5	133	2	US-08-624-735E-6	Sequence 6, Appli
39	484	22.0	125	2	US-08-624-735E-7	Sequence 7, Appli
40	429	19.5	80	2	US-08-624-735E-8	Sequence 8, Appli
41	427	19.4	225	2	US-09-949-016-11719	Sequence 11719, A
42	407.5	18.5	388	2	US-09-248-796A-19306	Sequence 19306, A
43	355.5	16.1	706	2	US-09-538-092-649	Sequence 649, App
44	342.5	15.6	341	2	US-09-902-540-15627	Sequence 15627, A
45	331	15.0	120	2	US-09-720-529A-6	Sequence 6, Appli

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Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYYDGD.....PEDAVHEDSGDEDGEDPDKR 405

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2202	100.0	498	5	US-10-803-575B-3	Sequence 3, Appli
2	2202	100.0	498	5	US-10-803-344B-3	Sequence 3, Appli
3	2202	100.0	498	5	US-10-803-580B-3	Sequence 3, Appli
4	2202	100.0	498	6	US-11-013-234-3	Sequence 3, Appli
5	2202	100.0	498	6	US-11-013-056-3	Sequence 3, Appli
6	2171	98.6	488	3	US-09-563-728A-26	Sequence 26, Appl
7	2171	98.6	488	4	US-10-177-293-206	Sequence 206, App
8	2171	98.6	488	4	US-10-360-534-2	Sequence 2, Appli
9	2171	98.6	488	5	US-10-723-860-2984	Sequence 2984, Ap
10	2144	97.4	488	5	US-10-941-947-6	Sequence 6, Appli
11	2105.5	95.6	489	3	US-09-817-913-3	Sequence 3, Appli
12	2105.5	95.6	489	3	US-09-817-538-3	Sequence 3, Appli
13	2105.5	95.6	489	5	US-10-870-587-3	Sequence 3, Appli
14	2047.5	93.0	482	3	US-09-563-728A-24	Sequence 24, Appl
15	2047.5	93.0	482	4	US-10-189-818B-7	Sequence 7, Appli
16	2047.5	93.0	482	4	US-10-360-534-1	Sequence 1, Appli

17	2047.5	93.0	482	5	US-10-756-149-5029	Sequence 5029, Ap
18	2047.5	93.0	488	3	US-09-925-300-1563	Sequence 1563, Ap
19	2047.5	93.0	513	5	US-10-803-575B-1	Sequence 1, Appli
20	2047.5	93.0	513	5	US-10-803-344B-1	Sequence 1, Appli
21	2047.5	93.0	513	5	US-10-803-580B-1	Sequence 1, Appli
22	2047.5	93.0	513	6	US-11-013-234-1	Sequence 1, Appli
23	2047.5	93.0	513	6	US-11-013-056-1	Sequence 1, Appli
24	2047.5	93.0	556	4	US-10-475-681-8	Sequence 8, Appli
25	2047.5	93.0	557	4	US-10-475-681-4	Sequence 4, Appli
26	2044.5	92.8	480	4	US-10-403-571-152	Sequence 152, App
27	2039.5	92.6	480	3	US-09-347-331-9	Sequence 9, Appli
28	2033.5	92.3	482	4	US-10-408-765A-222	Sequence 222, App
29	2031	92.2	481	3	US-09-817-913-1	Sequence 1, Appli
30	2031	92.2	481	3	US-09-817-538-1	Sequence 1, Appli
31	2031	92.2	481	5	US-10-870-587-1	Sequence 1, Appli
32	2027	92.1	481	5	US-10-941-947-5	Sequence 5, Appli
33	1953.5	88.7	576	3	US-09-347-331-11	Sequence 11, Appl
34	1913.5	86.9	492	5	US-10-450-763-47474	Sequence 47474, A
35	1908	86.6	521	6	US-11-097-143-87	Sequence 87, Appl
36	1573.5	71.5	461	4	US-10-369-493-6602	Sequence 6602, Ap
37	1537	69.8	518	4	US-10-321-732-13	Sequence 13, Appl
38	1537	69.8	518	6	US-11-087-099-9771	Sequence 9771, Ap
39	1537	69.8	528	4	US-10-437-963-174015	Sequence 174015,
40	1535.5	69.7	471	6	US-11-024-959-419	Sequence 419, App
41	1535.5	69.7	497	6	US-11-087-099-4744	Sequence 4744, Ap
42	1532.5	69.6	494	6	US-11-087-099-12046	Sequence 12046, A
43	1532	69.6	439	3	US-09-883-720-6	Sequence 6, Appli
44	1532	69.6	496	4	US-10-425-115-361464	Sequence 361464,
45	1532	69.6	496	6	US-11-087-099-6702	Sequence 6702, Ap

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OM protein - protein search, using sw model

Run on: June 24, 2006, 00:33:23 ; Search time 22 Seconds
 (without alignments)
 420.566 Million cell updates/sec

Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYYDGD.....PEDAVHEDSGDEDGEDPDKR 405

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications_AA_New:*
 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	2171	98.6	488	6	US-10-528-104-1	Sequence 1, Appli
2	1537	69.8	460	6	US-10-449-902-46025	Sequence 46025, A
3	1537	69.8	518	6	US-10-449-902-46682	Sequence 46682, A
4	1504.5	68.3	519	6	US-10-953-349-26716	Sequence 26716, A
5	1504.5	68.3	542	6	US-10-953-349-26715	Sequence 26715, A
6	1480.5	67.2	509	6	US-10-449-902-55980	Sequence 55980, A
7	1417	64.4	430	6	US-10-449-902-44586	Sequence 44586, A
8	1385.5	62.9	476	6	US-10-953-349-26717	Sequence 26717, A
9	906	41.1	456	6	US-10-449-902-35613	Sequence 35613, A
10	765.5	34.8	299	6	US-10-449-902-35326	Sequence 35326, A
11	567	25.7	219	6	US-10-449-902-49310	Sequence 49310, A
12	412.5	18.7	216	6	US-10-953-349-24208	Sequence 24208, A
13	399.5	18.1	396	6	US-10-471-571A-914	Sequence 914, App
14	358.5	16.3	202	6	US-10-953-349-24209	Sequence 24209, A

15	310.5	14.1	396	6	US-10-953-349-27963	Sequence 27963, A
16	310.5	14.1	407	6	US-10-953-349-33271	Sequence 33271, A
17	310.5	14.1	468	6	US-10-953-349-3782	Sequence 3782, Ap
18	310.5	14.1	499	6	US-10-953-349-3781	Sequence 3781, Ap
19	310.5	14.1	552	6	US-10-953-349-3780	Sequence 3780, Ap
20	308	14.0	392	6	US-10-449-902-51317	Sequence 51317, A
21	308	14.0	392	6	US-10-449-902-55674	Sequence 55674, A
22	303	13.8	364	6	US-10-953-349-7143	Sequence 7143, Ap
23	303	13.8	377	6	US-10-953-349-7142	Sequence 7142, Ap
24	303	13.8	398	6	US-10-953-349-7141	Sequence 7141, Ap
25	302	13.7	391	6	US-10-953-349-31895	Sequence 31895, A
26	295.5	13.4	362	6	US-10-953-349-31896	Sequence 31896, A
27	290.5	13.2	314	7	US-11-293-697-3367	Sequence 3367, Ap
28	287.5	13.1	327	6	US-10-953-349-31897	Sequence 31897, A
29	274.5	12.5	744	6	US-10-449-902-41371	Sequence 41371, A
30	272.5	12.4	876	7	US-11-293-697-2981	Sequence 2981, Ap
31	269	12.2	338	6	US-10-953-349-27965	Sequence 27965, A
32	269	12.2	339	6	US-10-953-349-33273	Sequence 33273, A
33	269	12.2	354	6	US-10-953-349-27964	Sequence 27964, A
34	269	12.2	355	6	US-10-953-349-33272	Sequence 33272, A
35	268	12.2	395	6	US-10-449-902-46161	Sequence 46161, A
36	242	11.0	352	6	US-10-449-902-53711	Sequence 53711, A
37	238.5	10.8	443	6	US-10-449-902-50745	Sequence 50745, A
38	201.5	9.2	162	6	US-10-953-349-24210	Sequence 24210, A
39	128	5.8	447	6	US-10-953-349-21373	Sequence 21373, A
40	108	4.9	967	6	US-10-449-902-41352	Sequence 41352, A
41	107	4.9	426	6	US-10-953-349-21374	Sequence 21374, A
42	89.5	4.1	466	6	US-10-953-349-32396	Sequence 32396, A
43	89.5	4.1	470	6	US-10-953-349-32395	Sequence 32395, A
44	89.5	4.1	475	6	US-10-953-349-32394	Sequence 32394, A
45	87	4.0	771	6	US-10-449-902-42840	Sequence 42840, A

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OM protein - protein search, using sw model

Run on: June 24, 2006, 00:26:43 ; Search time 41 Seconds
 (without alignments)
 950.434 Million cell updates/sec

Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYDGI.....PEDAVHEDSGDEDGEDPDKR 405

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2025	92.0	480	1	S60381	RPD3 protein homol
2	1573.5	71.5	461	2	T20163	hypothetical prote
3	1529.5	69.5	465	2	T23963	hypothetical prote
4	1494.5	67.9	501	2	T05640	histone deacetylas
5	1481	67.3	513	2	T01413	probable histone d
6	1468	66.7	433	1	S22284	transcription regu
7	1419.5	64.5	424	2	JC7102	histone deacetylas
8	1417	64.4	405	2	T40300	histone deacetylas
9	1412.5	64.1	428	2	JC5834	histone deacetylas
10	1355	61.5	419	2	T47443	hypothetical prote
11	1196	54.3	434	2	T11643	histone deacetylas
12	1117.5	50.7	452	2	S64211	probable transcrip
13	1044	47.4	507	2	T19067	hypothetical prote
14	803.5	36.5	374	2	G90100	histone deacetylas
15	474.5	21.5	375	2	D70388	acetoin utilizatio
16	471	21.4	351	2	C90142	acetylpolysamine am
17	465.5	21.1	387	1	S39643	acetate / acetoin
18	460	20.9	470	2	S54089	hypothetical prote

19	428.5	19.5	389	2	E84054	acetoin dehydrogen
20	399.5	18.1	389	2	C89958	acetoin utilizatio
21	398.5	18.1	367	2	T36278	hypothetical prote
22	379.5	17.2	158	2	T48929	hypothetical prote
23	368	16.7	359	1	B69266	acetylpolyamine am
24	355.5	16.1	706	2	S62933	hypothetical prote
25	338.5	15.4	348	2	F90264	acetoin utilizatio
26	325	14.8	310	1	A70481	acetoin utilizatio
27	314.5	14.3	142	2	T47441	hypothetical prote
28	299.5	13.6	878	2	T17245	hypothetical prote
29	289	13.1	380	2	D83174	probable acetylpol
30	284	12.9	687	2	T43797	probable histone d
31	274	12.4	425	2	G86217	protein T27G7.14 [
32	272.5	12.4	1063	2	T46284	hypothetical prote
33	268.5	12.2	796	2	T32425	hypothetical prote
34	268	12.2	305	2	AG2224	histone deacetylas
35	268	12.2	310	2	B47050	glnA 3'-region hyp
36	267.5	12.1	335	1	H71071	hypothetical prote
37	262.5	11.9	338	2	H84173	acetoin utilizatio
38	262.5	11.9	343	1	G64366	acetylpolyamine am
39	262.5	11.9	1095	2	T13964	probable histone d
40	259.5	11.8	337	2	AB3440	acetylspermidine d
41	247.5	11.2	334	2	B75095	probable histone d
42	242	11.0	344	2	B83605	probable acetylpol
43	236	10.7	331	1	C69026	acetylpolyamine am
44	235	10.7	359	2	T05998	hypothetical prote
45	231.5	10.5	385	2	A81926	hypothetical prote

<http://es.ScoreAccessWeb/GetItem.action?AppId=10826170&seqId=545790&ItemName=us...> 8/28/06

5	2172	98.6	447	2	Q7SYZ5_XENLA	Q7syz5 xenopus lae
6	2146	97.5	488	1	HDAC2_CHICK	P56519 gallus gall
7	2064.5	93.8	480	2	Q5BL48_XENTR	Q5bl48 xenopus tro
8	2055.5	93.3	480	1	HDA1B_XENLA	O42227 xenopus lae
9	2055.5	93.3	480	2	Q7ZYT5_XENLA	Q7zyt5 xenopus lae
10	2053.5	93.3	482	1	HDAC1_MOUSE	O09106 mus musculu
11	2053.5	93.3	482	2	Q32PJ8_BOVIN	Q32pj8 bos taurus
12	2053.5	93.3	482	2	Q4QQW4_RAT	Q4qqw4 rattus norv
13	2053.5	93.3	482	2	Q58E49_MOUSE	Q58e49 mus musculu
14	2047.5	93.0	482	1	HDAC1_HUMAN	Q13547 homo sapien
15	2047.5	93.0	482	2	Q6IT96_HUMAN	Q6it96 homo sapien
16	2047.5	93.0	482	2	Q5RAG0_PONPY	Q5rag0 pongo pygma
17	2044.5	92.8	480	2	Q8JIY7_BRARE	Q8jiy7 brachydanio
18	2044	92.8	477	2	Q8QGJ8_FUGRU	Q8qgj8 fugu rubrip
19	2043.5	92.8	480	2	Q5RKQ4_BRARE	Q5rkq4 brachydanio
20	2039.5	92.6	480	1	HDAC1_CHICK	P56517 gallus gall
21	2025	92.0	480	1	HDA1A_XENLA	Q91695 xenopus lae
22	2025	92.0	480	2	Q66IY9_XENLA	Q66iy9 xenopus lae
23	2003	91.0	490	2	Q4T0U0_TETNG	Q4t0u0 tetraodon n
24	1953.5	88.7	576	1	HDAC1_STRPU	P56518 strongyloce
25	1951	88.6	486	2	Q4RNX4_TETNG	Q4rnx4 tetraodon n
26	1908	86.6	521	1	HDAC1_DROME	Q94517 drosophila
27	1901	86.3	457	2	Q6P2A8_BRARE	Q6p2a8 brachydanio
28	1901	86.3	466	2	Q7Q5D2_ANOGA	Q7q5d2 anopheles g
29	1633.5	74.2	579	2	Q8T7M1_PHYPO	Q8t7m1 physarum po
30	1597.5	72.5	495	2	Q55FN5_DICDI	Q55fn5 dictyosteli
31	1573.5	71.5	461	1	HDA1_CAEEL	O17695 caenorhabdi
32	1567.5	71.2	455	2	Q61W33_CAEER	Q61w33 caenorhabdi
33	1537	69.8	460	2	Q5VP94_ORYSA	Q5vp94 oryza sativ
34	1537	69.8	518	2	Q7Y0Y8_ORYSA	Q7y0y8 oryza sativ
35	1530	69.5	304	2	Q8BQ10_MOUSE	Q8bq10 mus musculu
36	1529.5	69.5	465	2	O62339_CAEEL	O62339 caenorhabdi
37	1527.5	69.4	458	2	Q60XF2_CAEER	Q60xf2 caenorhabdi
38	1515	68.8	517	2	Q94F82_MAIZE	Q94f82 zea mays (m
39	1511.5	68.6	688	2	Q4WI19_AS PFU	Q4wi19 aspergillus
40	1507.5	68.5	687	2	Q9P4F5_EMENI	Q9p4f5 emericella
41	1507.5	68.5	687	2	Q5B4N7_EMENI	Q5b4n7 aspergillus
42	1505.5	68.4	432	2	Q96VP0_KLULA	Q96vp0 kluyveromyc
43	1503.5	68.3	432	2	Q6CPV2_KLULA	Q6cpv2 kluyveromyc
44	1503.5	68.3	433	2	Q6FXA7_CANGA	Q6fxa7 candida gla
45	1501	68.2	493	2	Q9AXF0_ORYSA	Q9axf0 oryza sativ

ALIGNMENTS

RESULT 1

HDAC2_HUMAN

ID HDAC2_HUMAN STANDARD; PRT; 488 AA.

AC Q92769; Q5SRI8; Q5SZ86; Q8NEH4;

DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.

DT 21-JUN-2005, sequence version 2.

DT 07-MAR-2006, entry version 55.

DE Histone deacetylase 2 (HD2).

GN Name=HDAC2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

GenCore version 5.1.9

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 24, 2006, 18:32:49 ; Search time 1266 Seconds
 (without alignments)
 3345.688 Million cell updates/sec

Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYDGDID.....PEDAVHEDSGDEDEDGDPDKR 405

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
 -Q=/abss/ABSSWEB_spool/US10826170/runat_23062006_111905_29748/app_query.fasta_1
 -DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
 -USER=US10826170@CGN_1_1_2019@runat_23062006_111905_29748 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2202	100.0	1497	13	ADS18116	Ads18116 DNA encod
2	2202	100.0	1497	14	AEA49481	Aea49481 Human his
3	2202	100.0	1497	14	AEB56252	Aeb56252 Histone d
4	2198	99.8	1997	6	ABI99512	Abi99512 Mouse isc
5	2177	98.9	1964	8	ACD13380	Acd13380 Human DNA
6	2177	98.9	2212	12	ADQ21788	Adq21788 Human sof
7	2177	98.9	2212	12	ADQ24203	Adq24203 Human sof
8	2171	98.6	1985	2	AAZ32066	Aaz32066 Human MET
9	2171	98.6	1985	4	AAC89555	Aac89555 Human his
10	2171	98.6	1985	5	AAC90323	Aac90323 U31814 cD
11	2171	98.6	1985	8	ABZ34831	Abz34831 Coding se
12	2171	98.6	1985	8	ACC50181	Acc50181 Breast ca
13	2171	98.6	1985	10	ADK67005	Adk67005 Gene #95
14	2171	98.6	1985	12	ADJ26987	Adj26987 Human his
15	2171	98.6	1985	12	ADQ20163	Adq20163 Human sof
16	2171	98.6	1985	13	ADR24762	Adr24762 Breast ca
17	2171	98.6	1985	14	ADZ09567	Adz09567 Human bre
18	2171	98.6	1985	15	AEF54866	Aef54866 Human his
19	2171	98.6	1985	15	AEF74876	Aef74876 Human pol
20	2158	98.0	1986	12	ADN49033	Adn49033 Human his
21	2152	97.7	1985	6	ABK87716	Abk87716 Human cDN
22	2152	97.7	1985	10	ADC21690	Adc21690 Human cDN
23	2152	97.7	1985	14	ADW12270	Adw12270 Human his
24	2047.5	93.0	1449	2	AAT86371	Aat86371 cDNA enco
25	2047.5	93.0	1542	13	ADS18114	Ads18114 DNA encod
26	2047.5	93.0	1542	14	AEA49479	Aea49479 Human his
27	2047.5	93.0	1542	14	AEB56250	Aeb56250 Histone d
28	2047.5	93.0	1611	4	AAC89554	Aac89554 Human his
29	2047.5	93.0	1671	8	ABS58329	Abs58329 DNA encod
30	2047.5	93.0	1674	8	ABS58325	Abs58325 DNA encod
31	2047.5	93.0	2091	8	ACD13379	Acd13379 Human DNA
32	2047.5	93.0	2091	8	ACC47996	Acc47996 Human his
33	2047.5	93.0	2091	10	ADK67004	Adk67004 Gene #94
34	2047.5	93.0	2091	12	ADN03711	Adn03711 Antipsori
35	2047.5	93.0	2091	13	ACN37339	Acn37339 Tumour-as
36	2047.5	93.0	2091	14	ADX08109	Adx08109 Cyclin-de
37	2047.5	93.0	2091	14	ADZ48951	Adz48951 Insulin s
38	2047.5	93.0	2091	15	AEF54865	Aef54865 Human his
39	2047.5	93.0	2098	10	ADI02675	Adi02675 Human cDN
40	2047.5	93.0	2163	3	AAF16188	Aaf16188 Human pro
41	2047.5	93.0	2378	5	ABV25106	Abv25106 Human pro
42	2044.5	92.8	2213	12	ADO57384	Ado57384 DNA encod
43	2033.5	92.3	1446	11	ADN31056	Adn31056 Human his
44	2033.5	92.3	1449	12	ADQ62712	Adq62712 Human his
45	2033.5	92.3	2091	6	ABK83674	Abk83674 Human cDN

GenCore version 5.1.9

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 24, 2006, 18:35:08 ; Search time 415 Seconds
 (without alignments)
 2739.033 Million cell updates/sec

Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYDGD.....PEDAVHEDSGDEDEDGDPDKR 405

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
 -Q=/abss/ABSSWEB_spool/US10826170/runat_23062006_111912_29839/app_query.fasta_1
 -DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -HOST=abss02p -USER=US10826170_CGN_1_1_541@runat_23062006_111912_29839
 -NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	2202	100.0	2242	3	US-09-949-016-1553	Sequence 1553, Ap
2	2047.5	93.0	1449	3	US-08-624-735E-1	Sequence 1, Appli
3	2033.5	92.3	2111	2	US-08-528-255A-2	Sequence 2, Appli
4	2033.5	92.3	2111	2	US-08-717-365-2	Sequence 2, Appli
5	1985	90.1	1969	3	US-09-949-016-5038	Sequence 5038, Ap
6	1532	69.6	2019	3	US-09-282-305-5	Sequence 5, Appli
7	1532	69.6	2019	3	US-09-883-720-5	Sequence 5, Appli
8	1515	68.8	1943	3	US-09-282-305-7	Sequence 7, Appli
9	1515	68.8	1943	3	US-09-883-720-7	Sequence 7, Appli
10	1509	68.5	1990	3	US-09-720-529A-1	Sequence 1, Appli
11	1495.5	67.9	1807	3	US-09-645-337A-1	Sequence 1, Appli
12	1489.5	67.6	1805	3	US-09-720-529A-3	Sequence 3, Appli
13	1483	67.3	1347	3	US-09-248-796A-5060	Sequence 5060, Ap
14	1461.5	66.4	1800	3	US-09-645-337A-3	Sequence 3, Appli
15	1416.5	64.3	1890	3	US-09-949-016-4302	Sequence 4302, Ap
16	1404.5	63.8	1826	3	US-09-282-305-1	Sequence 1, Appli
17	1404.5	63.8	1826	3	US-09-883-720-1	Sequence 1, Appli
18	1385	62.9	1524	3	US-09-248-796A-5061	Sequence 5061, Ap
19	1385	62.9	1576	3	US-09-282-305-9	Sequence 9, Appli
20	1385	62.9	1576	3	US-09-883-720-9	Sequence 9, Appli
21	1134	51.5	1365	3	US-09-248-796A-5202	Sequence 5202, Ap
22	1017	46.2	1475	3	US-09-282-305-3	Sequence 3, Appli
23	1017	46.2	1475	3	US-09-883-720-3	Sequence 3, Appli
24	829	37.6	1682	3	US-10-239-333B-1	Sequence 1, Appli
25	796.5	36.2	1709	3	US-09-949-016-5848	Sequence 5848, Ap
26	746	33.9	841	3	US-08-998-416-317	Sequence 317, App
27	637.5	29.0	35493	3	US-09-949-016-16780	Sequence 16780, A
28	484	22.0	375	3	US-08-624-735E-3	Sequence 3, Appli
29	484	22.0	379	3	US-08-624-735E-2	Sequence 2, Appli
30	472.5	21.5	570	3	US-09-533-559-63	Sequence 63, Appl
c 31	472	21.4	1558	3	US-09-949-016-5115	Sequence 5115, Ap
32	418	19.0	227	3	US-08-624-735E-4	Sequence 4, Appli
33	409	18.6	34629	3	US-09-949-016-13295	Sequence 13295, A
34	408	18.5	383	3	US-08-624-735E-18	Sequence 18, Appl
35	407.5	18.5	1164	3	US-09-248-796A-5203	Sequence 5203, Ap
c 36	399.5	18.1	12173	3	US-08-956-171E-310	Sequence 310, App
c 37	399.5	18.1	12173	3	US-08-781-986A-310	Sequence 310, App
38	398.5	18.1	1017	5	US-09-974-300-4355	Sequence 4355, Ap
39	382	17.3	313	3	US-08-624-735E-20	Sequence 20, Appl
40	374	17.0	241	3	US-09-389-681-403	Sequence 403, App
41	374	17.0	241	3	US-09-620-405B-403	Sequence 403, App
42	374	17.0	241	3	US-09-433-826B-403	Sequence 403, App
43	374	17.0	241	3	US-09-604-287A-403	Sequence 403, App
44	374	17.0	241	3	US-09-834-759-403	Sequence 403, App
45	374	17.0	241	3	US-09-590-751A-403	Sequence 403, App

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2006, 09:17:55 ; Search time 7472 Seconds
 (without alignments)
 5199.151 Million cell updates/sec

Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYYDGDID.....PEDAVHEDSGDEDGEDPDKR 405

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
 -Q=/abss/ABSSWEB_spool/US10826170/runat_23062006_111906_29759/app_query.fasta_1
 -DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
 -USER=US10826170@CGN_1_1_5548@runat_23062006_111906_29759 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
 1: gb_env:*
 2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2202	100.0	1497	2	CS131549	CS131549 Sequence
2	2202	100.0	1497	2	CS131933	CS131933 Sequence
3	2202	100.0	1966	2	CQ719196	CQ719196 Sequence
4	2198	99.8	1997	2	AX305742	AX305742 Sequence
5	2198	99.8	1997	6	MMU31758	U31758 Mus musculu
6	2197	99.8	1467	8	AY892979	AY892979 Synthetic
7	2197	99.8	2074	5	BC031055	BC031055 Homo sapi
8	2193	99.6	1467	6	AB221663	AB221663 Mus muscu
9	2181	99.0	1963	11	CR926395	CR926395 Xenopus t
10	2181	99.0	2044	11	BC074509	BC074509 Xenopus t
11	2177	98.9	1910	11	BC081054	BC081054 Xenopus l
12	2172	98.6	1536	11	BC054208	BC054208 Xenopus l
13	2171	98.6	1985	2	BD129612	BD129612 Polynucle
14	2171	98.6	1985	2	CQ796378	CQ796378 Sequence
15	2171	98.6	1985	2	CS063027	CS063027 Sequence
16	2171	98.6	1985	2	CS080808	CS080808 Sequence
17	2171	98.6	1985	2	AX053103	AX053103 Sequence
18	2171	98.6	1985	2	AX578067	AX578067 Sequence
19	2171	98.6	1985	2	AX821967	AX821967 Sequence
20	2171	98.6	1985	5	HSU31814	U31814 Human trans
21	2161.5	98.2	2056	5	AK097376	AK097376 Homo sapi
22	2152	97.7	1985	2	AX703600	AX703600 Sequence
23	2146	97.5	1878	11	AF039752	AF039752 Gallus ga
24	2104	95.5	2000	5	AK092156	AK092156 Homo sapi
25	2068.5	93.9	2247	11	CT030593	CT030593 Xenopus t
26	2064.5	93.8	1850	11	BC090604	BC090604 Xenopus t
27	2055.5	93.3	1487	11	AF020658	AF020658 Xenopus l
28	2055.5	93.3	2227	11	BC041296	BC041296 Xenopus l
29	2053.5	93.3	1385	6	BC059156	BC059156 Rattus no
30	2053.5	93.3	1977	6	MMHIDE	X98207 M.musculus
31	2053.5	93.3	1978	6	BC092070	BC092070 Mus muscu
32	2053.5	93.3	1992	6	BC108371	BC108371 Mus muscu
33	2053.5	93.3	2025	14	BC108088	BC108088 Bos tauru
34	2053.5	93.3	2033	6	BC107476	BC107476 Rattus no
35	2053.5	93.3	2035	6	BC097943	BC097943 Rattus no
36	2047.5	93.0	1449	2	AR576966	AR576966 Sequence
37	2047.5	93.0	1449	5	CR541717	CR541717 Homo sapi
38	2047.5	93.0	1449	8	AY890400	AY890400 Synthetic
39	2047.5	93.0	1449	8	AY891420	AY891420 Synthetic
40	2047.5	93.0	1449	8	AY893265	AY893265 Synthetic
41	2047.5	93.0	1449	8	BT007472	BT007472 Synthetic
42	2047.5	93.0	1464	5	AY627042	AY627042 Homo sapi
43	2047.5	93.0	1542	2	CS131547	CS131547 Sequence
44	2047.5	93.0	1542	2	CS131931	CS131931 Sequence
45	2047.5	93.0	1611	2	CQ767178	CQ767178 Sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2006, 08:39:30 ; Search time 2374 Seconds
 (without alignments)
 3144.372 Million cell updates/sec

Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYYDGD.....PEDAVHEDSGDEDGEDPDKR 405

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
 -Q=/abss/ABSSWEB_spool/US10826170/runat_23062006_111915_29906/app_query.fasta_1
 -DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
 -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
 -USER=US10826170_CGN_1_1_4066_@runat_23062006_111915_29906 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2202	100.0	1497	9	US-10-803-575B-4	Sequence 4, Appli
2	2202	100.0	1497	9	US-10-803-344B-4	Sequence 4, Appli
3	2202	100.0	1497	10	US-10-803-580B-4	Sequence 4, Appli
4	2202	100.0	1497	13	US-11-013-234-4	Sequence 4, Appli
5	2202	100.0	1497	13	US-11-013-056-4	Sequence 4, Appli
6	2177	98.9	2212	9	US-10-723-860-4608	Sequence 4608, Ap
7	2177	98.9	2212	9	US-10-723-860-7023	Sequence 7023, Ap
8	2171	98.6	1985	3	US-09-563-728A-27	Sequence 27, Appl
9	2171	98.6	1985	3	US-09-373-658-76	Sequence 76, Appl
10	2171	98.6	1985	3	US-09-989-687-76	Sequence 76, Appl
11	2171	98.6	1985	7	US-10-177-293-205	Sequence 205, App
12	2171	98.6	1985	7	US-10-172-118-623	Sequence 623, App
13	2171	98.6	1985	7	US-10-173-192-4	Sequence 4, Appli
14	2171	98.6	1985	8	US-10-342-887-623	Sequence 623, App
15	2171	98.6	1985	8	US-10-653-528-4	Sequence 4, Appli
16	2171	98.6	1985	9	US-10-723-860-2983	Sequence 2983, Ap
17	2171	98.6	1985	9	US-10-473-974-189	Sequence 189, App
18	2171	98.6	1985	10	US-10-504-173-95	Sequence 95, Appl
19	2171	98.6	1985	16	US-11-245-147-189	Sequence 189, App
20	2152	97.7	1985	3	US-09-817-913-4	Sequence 4, Appli
21	2152	97.7	1985	3	US-09-817-538-4	Sequence 4, Appli
22	2152	97.7	1985	9	US-10-870-587-4	Sequence 4, Appli
23	2047.5	93.0	1542	9	US-10-803-575B-2	Sequence 2, Appli
24	2047.5	93.0	1542	9	US-10-803-344B-2	Sequence 2, Appli
25	2047.5	93.0	1542	10	US-10-803-580B-2	Sequence 2, Appli
26	2047.5	93.0	1542	13	US-11-013-234-2	Sequence 2, Appli
27	2047.5	93.0	1542	13	US-11-013-056-2	Sequence 2, Appli
28	2047.5	93.0	1611	3	US-09-563-728A-25	Sequence 25, Appl
29	2047.5	93.0	1611	8	US-10-189-818B-6	Sequence 6, Appli
30	2047.5	93.0	1611	10	US-10-756-149-1241	Sequence 1241, Ap
31	2047.5	93.0	1671	8	US-10-475-681-16	Sequence 16, Appl
32	2047.5	93.0	1674	8	US-10-475-681-12	Sequence 12, Appl
33	2047.5	93.0	2091	10	US-10-492-901-12	Sequence 12, Appl
34	2047.5	93.0	2091	10	US-10-887-553A-280	Sequence 280, App
35	2047.5	93.0	2091	10	US-10-504-173-94	Sequence 94, Appl
36	2047.5	93.0	2098	7	US-10-133-013-216	Sequence 216, App
37	2047.5	93.0	2163	3	US-09-925-300-623	Sequence 623, App
38	2047.5	93.0	2197	7	US-10-062-674-1925	Sequence 1925, Ap
39	2047.5	93.0	2378	9	US-10-357-930-25095	Sequence 25095, A
40	2044.5	92.8	2213	8	US-10-403-571-151	Sequence 151, App
41	2033.5	92.3	2091	4	US-09-745-167A-3	Sequence 3, Appli
42	2033.5	92.3	2091	10	US-10-977-291-3	Sequence 3, Appli
43	2025.5	92.0	1611	3	US-09-817-913-2	Sequence 2, Appli
44	2025.5	92.0	1611	3	US-09-817-538-2	Sequence 2, Appli
45	2025.5	92.0	1611	9	US-10-870-587-2	Sequence 2, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2006, 09:32:55 ; Search time 65 Seconds
 (without alignments)
 2240.505 Million cell updates/sec

Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYDGD.....PEDAVHEDSGDEDEDPDKR 405

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10826170/runat_23062006_111918_29962/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss06p
-USER=US10826170_@CGN_1_1_45_@runat_23062006_111918_29962 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
 Result Query

No.	Score	Match	Length	DB	ID	Description
1	2171	98.6	1985	6	US-10-528-104-5	Sequence 5, Appli
2	1537	69.8	2119	6	US-10-449-902-18278	Sequence 18278, A
3	1537	69.8	2511	6	US-10-449-902-17618	Sequence 17618, A
4	1504.5	68.3	1798	6	US-10-953-349-26714	Sequence 26714, A
5	1480.5	67.2	1942	6	US-10-449-902-27655	Sequence 27655, A
6	1467	66.6	1302	7	US-11-217-529-78173	Sequence 78173, A
7	1456	66.1	1302	7	US-11-217-529-2080	Sequence 2080, Ap
8	1417	64.4	1715	6	US-10-449-902-16162	Sequence 16162, A
9	1207	54.8	1929	6	US-10-449-902-6866	Sequence 6866, Ap
10	1121.5	50.9	1359	7	US-11-217-529-76545	Sequence 76545, A
11	906	41.1	1756	6	US-10-449-902-7153	Sequence 7153, Ap
12	567	25.7	938	6	US-10-449-902-20927	Sequence 20927, A
13	459.5	20.9	1419	7	US-11-217-529-2682	Sequence 2682, Ap
14	454.5	20.6	1185	7	US-11-217-529-81583	Sequence 81583, A
15	412.5	18.7	900	6	US-10-953-349-24207	Sequence 24207, A
16	399.5	18.1	1188	6	US-10-471-571A-913	Sequence 913, App
17	349.5	15.9	1926	7	US-11-217-529-81124	Sequence 81124, A
18	343.5	15.6	2121	7	US-11-217-529-2220	Sequence 2220, Ap
19	310.5	14.1	1476	6	US-10-953-349-27962	Sequence 27962, A
20	310.5	14.1	1794	6	US-10-953-349-33270	Sequence 33270, A
21	310.5	14.1	1991	6	US-10-953-349-3779	Sequence 3779, Ap
22	308	14.0	2171	6	US-10-449-902-22948	Sequence 22948, A
23	308	14.0	2802	6	US-10-449-902-27344	Sequence 27344, A
24	303	13.8	1358	6	US-10-953-349-7140	Sequence 7140, Ap
25	302	13.7	1506	6	US-10-953-349-31894	Sequence 31894, A
26	290.5	13.2	2421	7	US-11-293-697-924	Sequence 924, App
27	275.5	12.5	3099	7	US-11-293-697-538	Sequence 538, App
28	274.5	12.5	3926	6	US-10-449-902-12925	Sequence 12925, A
29	268	12.2	1471	6	US-10-449-902-17754	Sequence 17754, A
30	242	11.0	1353	6	US-10-449-902-25370	Sequence 25370, A
31	240	10.9	1742	6	US-10-449-902-22371	Sequence 22371, A
32	145	6.6	1625	6	US-10-953-349-21372	Sequence 21372, A
33	117.5	5.3	2100	7	US-11-217-529-2593	Sequence 2593, Ap
34	108	4.9	3004	6	US-10-449-902-12906	Sequence 12906, A
35	103.5	4.7	822	7	US-11-217-529-82719	Sequence 82719, A
36	91.5	4.2	909	7	US-11-217-529-397	Sequence 397, App
37	89.5	4.1	1613	6	US-10-953-349-32393	Sequence 32393, A
38	88.5	4.0	1770	7	US-11-217-529-2290	Sequence 2290, Ap
39	87	4.0	2840	6	US-10-449-902-14400	Sequence 14400, A
40	86.5	3.9	1761	6	US-10-449-902-21296	Sequence 21296, A
c 41	86	3.9	1167	7	US-11-217-529-2761	Sequence 2761, Ap
42	86	3.9	3108	7	US-11-217-529-76535	Sequence 76535, A
43	86	3.9	3589	6	US-10-449-902-25267	Sequence 25267, A
44	85.5	3.9	2757	7	US-11-217-529-1647	Sequence 1647, Ap
45	85	3.9	1755	7	US-11-217-529-78469	Sequence 78469, A

GenCore version 5.1.9

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2006, 09:23:52 ; Search time 6133 Seconds
 (without alignments)
 5539.050 Million cell updates/sec

Title: US-10-826-170-5
 Perfect score: 2202
 Sequence: 1 MAYSQGGGKKKVCYYYDGDID.....PEDAVHEDSGDEDEDGPDKR 405

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
 -Q=/abss/ABSSWEB_spool/US10826170/runat_23062006_111909_29770/app_query.fasta_1
 -DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
 -USER=US10826170@CGN_1_1_6323@runat_23062006_111909_29770 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
 1: gb_est1:*
 2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2202	100.0	1955	6	CR610322	CR610322 full-leng
2	2193	99.6	1627	6	BC013141	BC013141 Homo sapi
3	2053.5	93.3	1407	6	BC092285	BC092285 Mus muscu
4	2047.5	93.0	2042	6	CR611580	CR611580 full-leng
5	2047.5	93.0	2066	6	CR859057	CR859057 Pongo pyg
6	1977	89.8	1467	14	AY409539	AY409539 Homo sapi
7	1977	89.8	1467	14	AY409541	AY409541 Mus muscu
8	1970	89.5	1467	14	AY409540	AY409540 Pan trogl
9	1948	88.5	2215	6	CNS0GRFZ	CR731594 Tetraodon
10	1926	87.5	1953	6	AK076080	AK076080 Mus muscu
11	1852.5	84.1	1406	10	DT993770	DT993770 CNB169-A0
12	1850.5	84.0	1908	6	CNS0GSXL	CR733738 Tetraodon
13	1817	82.5	1398	14	AY420900	AY420900 Homo sapi
14	1745	79.2	1121	9	DN705006	DN705006 CLJ56-G08
15	1732	78.7	1016	5	CF109194	CF109194 Shultzomi
16	1717	78.0	1488	9	DN737685	DN737685 CNB94-C01
17	1695.5	77.0	1491	9	DN714751	DN714751 CNB104-D0
18	1682	76.4	1114	5	CD506374	CD506374 CDA78-H05
19	1665.5	75.6	1277	9	DN724933	DN724933 CNB22-A05
20	1664	75.6	1146	9	DN719749	DN719749 CNB13-H04
21	1658	75.3	1069	10	DW667381	DW667381 CNB342-C1
22	1652.5	75.0	1108	10	DW028453	DW028453 CFW245-E0
23	1650	74.9	1138	10	DV009383	DV009383 CNB257-E0
24	1645	74.7	1114	10	DW608031	DW608031 CGX192-G0
25	1629.5	74.0	1141	10	DW619200	DW619200 CLJ309-C0
26	1627.5	73.9	1110	10	DW619490	DW619490 CLJ311-A0
27	1623.5	73.7	1341	9	DN717007	DN717007 CNB116-A1
28	1618	73.5	1142	4	BX425368	BX425368 BX425368
29	1611	73.2	977	10	DW635911	DW635911 CLJ365-D0
30	1610	73.1	1287	14	AY420902	AY420902 Mus muscu
31	1605	72.9	1123	10	DV013481	DV013481 CNB280-E1
32	1598	72.6	961	8	CO649034	CO649034 ILLUMIGEN
33	1597	72.5	959	10	DT448333	DT448333 JGI_CABK7
34	1589.5	72.2	1398	10	DT991274	DT991274 CNB154-F0
35	1581	71.8	894	8	CR578170	CR578170 CR578170
36	1580	71.8	1274	10	DT956210	DT956210 CFW144-A1
37	1577.5	71.6	1384	9	DN700114	DN700114 CLJ27-F05
38	1576.5	71.6	982	10	DV007084	DV007084 CNB244-F0
39	1569.5	71.3	999	4	BX421673	BX421673 BX421673
40	1569	71.3	963	8	CO550659	CO550659 LyEST8921
41	1568	71.2	907	10	DT811651	DT811651 LB01615.C
42	1566.5	71.1	1084	10	DW614476	DW614476 CLJ281-A0
43	1561.5	70.9	1091	1	AL531607	AL531607 AL531607
44	1556	70.7	1407	9	DN736843	DN736843 CNB89-D06
45	1550	70.4	988	2	BM468325	BM468325 AGENCOURT